

Title (en)
COMPOSITIONS AND METHODS FOR IMPROVING BASE EDITING

Title (de)
ZUSAMMENSETZUNGEN UND VERFAHREN ZUR VERBESSERTEN BASISBEARBEITUNG

Title (fr)
COMPOSITIONS ET PROCÉDÉS D'AMÉLIORATION DE L'ÉDITION DE BASE

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Application
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Abstract (en)
[origin: WO2020051562A2] The invention features compositions and methods for modifying a polynucleotide (e.g., DNA) using a nucleobase editor comprising a first DNA binding protein domain that is catalytically inactive, a domain having base editing activity, and a second DNA binding protein domain having nickase activity, where the DNA binding protein domains are expressed as a single fusion protein or are expressed separately (e.g., on separate expression vectors). The invention also features a fusion protein comprising a domain having base editing activity (e.g., cytidine deaminase or adenosine deaminase), and two nucleic acid programmable DNA binding protein domains (napDNAbp), a first napDNAbp comprising nickase activity and a second napDNAbp that is catalytically inactive, where at least the two napDNAbps are joined by a linker. In one embodiment, the fusion protein comprises a DNA binding domain of a CRISPR-Cas having nickase activity (nCas; e.g., nCas9), a catalytically inactive DNA binding domain of CRISPR-Cas (dCas; e.g., dCas9), and a deaminase domain, where the dCas is joined to the nCas by a linker, and the dCas is immediately adjacent to the deaminase domain, as well as related methods for using such base editors, and kits comprising the base editors.

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Citation (search report)
• [XY] WO 2018129129 A1 20180712 - UNIV RUTGERS [US]
• [AD] GAUDELLI NICOLE M ET AL: "Programmable base editing of A-T to G-C in genomic DNA without DNA cleavage", NATURE, NATURE PUBLISHING GROUP UK, LONDON, vol. 551, no. 7681, 23 November 2017 (2017-11-23), pages 464 - 471, XP037336615, ISSN: 0028-0836, DOI: 10.1038/NATURE24644
• [YA] BOLUKBASI MEHMET FATIH ET AL: "DNA-binding-domain fusions enhance the targeting range and precision of Cas9", NATURE METHODS, vol. 12, no. 12, 19 October 2015 (2015-10-19), New York, pages 1150 - 1156, XP093012024, ISSN: 1548-7091, DOI: 10.1038/nmeth.3624
• [A] AYMAN EID ET AL: "CRISPR base editors: genome editing without double-stranded breaks", BIOCHEMICAL JOURNAL, vol. 475, no. 11, 11 June 2018 (2018-06-11), GB, pages 1955 - 1964, XP055638645, ISSN: 0264-6021, DOI: 10.1042/BCJ20170793
• [AD] ALEXIS C. KOMOR ET AL: "Improved base excision repair inhibition and bacteriophage Mu Gam protein yields C:G-to-T:A base editors with higher efficiency and product purity", SCIENCE ADVANCES, vol. 3, no. 8, 1 August 2017 (2017-08-01), pages eaao4774, XP055453964, DOI: 10.1126/sciadv.aao4774
• See references of WO 2020051562A2

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